

# SEQUENCE LISTING

<110> FREY, Perry A.  
RUZICKA, Frank J.

<120> DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE

<130> 032026/0476

<140> US 09/330,611

<141> 1999-06-11

<150> US 09/198,942

<151> 1998-11-24

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<170> PatentIn Ver. 2.0

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Tyr Pro Asp Arg Val Leu Leu Leu Ile Thr Asp Met Cys Ser Met Tyr
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Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro	
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 Lys Gly Asn Pro Gln Asp Pro Leu Phe Leu Gln Val Met Cys Ser Asp  
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Leu Glu Phe Val Gln Ala Glu Gly Phe Ser Thr Asp Pro Leu Glu Glu  
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Lys Asn Ala Asn Ala Val Pro Asn Ile Leu His Lys Tyr Arg Asn Arg  
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Phe Arg Arg His Phe Pro Tyr Asp Glu Asn Pro Gly Asn Lys Lys Ser  
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Val Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu  
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Arg Ile His Thr Arg Leu Pro Val Val Ile Pro Gln Arg Ile Thr Asp  
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Thr His Ile Asn His Pro Asn Glu Ile Asp Gln Ile Phe Ala His Ala  
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cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctt	624
Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu	
195 200 205	
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat	672
Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His	
210 215 220	
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa	720
Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu	
225 230 235 240	
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg	768
Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu	
245 250 255	

ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg 816  
Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
260 265 270

atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac 864  
Met Lys Arg Leu Val His Leu Val Lys Met Arg Val Arg Pro Tyr  
275 280 285

tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg 912  
Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
290 295 300

ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc 960  
Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
305 310 315 320

tcg ggc tat gct gtt cct acc ttt gtg gta gat gct ccg ggg ggt ggt 1008  
Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly  
325 330 335

ggt aag ata cct gta atg ccg aac tat gtt gta tct cag tcc cca cga 1056  
Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
340 345 350

cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag 1104  
His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Tyr Thr Glu  
355 360 365

ccg gag aat tat cat gag gag tgt gat tgt gag gac tgt cga gcc ggt 1152  
Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
370 375 380

aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct 1200  
Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Leu Ala  
385 390 395 400

atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac 1248  
Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
405 410 415

tga 1251

<210> 8  
<211> 416  
<212> PRT  
<213> Porphyromonas gingivalis

<400> 8  
Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu  
1 5 10 15

Gln Trp Asn Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu  
20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu  
35 40 45

Val Lys Glu Ser Leu Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr  
50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln  
65 70 75 80

Ala Ile Pro Thr His Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val  
85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His  
100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met  
115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala  
130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn  
145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu  
165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile  
180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu  
195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His  
210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu  
225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu  
245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val  
260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr  
275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr  
290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr  
305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly  
325 330 335

Gly Lys Ile Pro Val Met Pro Asn Tyr Val Val Ser Gln Ser Pro Arg  
340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu  
355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly  
370 375 380

Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala  
385 390 395 400

Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn  
405 410 415

<210> 9  
 <211> 1416  
 <212> DNA  
 <213> Bacillus subtilis

<220>  
 <221> CDS  
 <222> (1)..(1413)

<400> 9  
 atg aaa aac aaa tgg tat aaa ccg aaa cgg cat tgg aag gag atc gag 48  
 Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu  
 1 5 10 15  
 tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96  
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30  
 ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144  
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45  
 ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192  
 Leu Thr Glu Asp Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60  
 ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240  
 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80  
 ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg 288  
 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Asp Glu Met  
 85 90 95  
 cac aaa aca aaa tac gat ctg gaa gac ccg ctt cat gag gat gaa gat 336  
 His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110  
 tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt 384  
 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125  
 ctt gtc acg aat caa tgt tcc atg tac tgc cgc tac tgc aca aga agg 432  
 Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg  
 130 135 140  
 cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat 480  
 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160  
 gct gca att gct tat atc ccg gaa aca ccc gaa atc cgc gat tgt tta 528  
 Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
 165 170 175  
 att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat 576  
 Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
 180 185 190  
 att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc aga atc 624  
 Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
 195 200 205

gga aca aga gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg	672
Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu	
210 215 220	
tcg gag ata ttg aaa tat cat ccg gtc tgg ctg aac acc cat ttt	720
Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe	
225 230 235 240	
aac aca agc atc gaa atg aca gaa gaa tcc gtt gag gca tgt gaa aag	768
Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys	
245 250 255	
ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca	816
Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala	
260 265 270	
ggg att aat gat tcg gtt cca att atg aaa aag ctc atg cat gac ttg	864
Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu	
275 280 285	
gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca	912
Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser	
290 295 300	
gaa gga ata ggg cat ttc aga gct cct gtt tcc aaa ggt ttg gag atc	960
Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile	
305 310 315 320	
att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt	1008
Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe	
325 330 335	
gtc gtt gac gca cca ggc gga gga ggt aaa atc gcc ctg cag cca aac	1056
Val Val Asp Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn	
340 345 350	
tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa	1104
Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu	
355 360 365	
ggg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag	1152
Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln	
370 375 380	
gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag	1200
Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys	
385 390 395 400	
gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt	1248
Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe	
405 410 415	
aca cct gaa aat gta gac aga atc aaa agg aga gag gca tac atc gca	1296
Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala	
420 425 430	
aat ccg gag cat gaa aca tta aaa gat ccg cgt gag aaa aga gat cag	1344
Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln	
435 440 445	
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act	1392
Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr	
450 455 460	

gaa tgc gga ggg gat tct tca tga  
 Glu Cys Gly Gly Asp Ser Ser  
 465 470

1416

<210> 10  
 <211> 471  
 <212> PRT  
 <213> Bacillus subtilis

<400> 10  
 Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu  
 1 5 10 15  
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln  
 20 25 30  
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn  
 35 40 45  
 Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile  
 50 55 60  
 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn  
 65 70 75 80  
 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met  
 85 90 95  
 His Lys Thr Lys Tyr Asp Leu Glu Asp Pro Leu His Glu Asp Glu Asp  
 100 105 110  
 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe  
 115 120 125  
 Leu Val Thr Asn Gln Cys Ser Met Tyr Cys Arg Tyr Cys Thr Arg Arg  
 130 135 140  
 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp  
 145 150 155 160  
 Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu  
 165 170 175  
 Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr  
 180 185 190  
 Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile  
 195 200 205  
 Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu  
 210 215 220  
 Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe  
 225 230 235 240  
 Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys  
 245 250 255  
 Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala  
 260 265 270  
 Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu  
 275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser  
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile  
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe  
325 330 335

Val Val Asp Ala Pro Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn  
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu  
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln  
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys  
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe  
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala  
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln  
435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr  
450 455 460

Glu Cys Gly Gly Asp Ser Ser  
465 470

<210> 11  
<211> 1188  
<212> DNA  
<213> Deinococcus radiodurans

<220>  
<221> CDS  
<222> (1)..(1188)

<400> 11  
tgg caa ggc gta ccc gac gag cag tgg tac gac tgg aaa tgg cag ctc 48  
Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu  
1 5 10 15  
aag aac cgc atc aac agt gtg gag gag ttg cag gaa gtc ctg acc ctc 96  
Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu  
20 25 30  
acc gag tcc gag tac cgg ggt gcg tcc gcc gag ggc att ttc cgc ctc 144  
Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu  
35 40 45  
gac atc acg ccg tat ttc gcg tcc ctc atg gac ccc gaa gac ccc acc 192  
Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr  
50 55 60



tgc ccg gtg cgc cgt cag gtg att ccc acc gag gag gag ctc cag ccg	240
Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Glu Leu Gln Pro	
65 70 75 80	
ttc acc tcc atg atg gaa gac tct ctc gcg gag gat aag cac tcg ccc	288
Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro	
85 90 95	
gtg ccg ggg ctg gtg cac cgc tac ccc gac cgc gtg ctg atg ctg gtc	336
Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val	
100 105 110	
acg acc cag tgc gcg agc tac tgc cgc tac tgc acc cga agc cgc atc	384
Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile	
115 120 125	
gtg ggc gac ccc acc gag acg ttc aat ccc gcc gag tat gag gcg cag	432
Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln	
130 135 140	
ctc aac tac ctg cgc aac acc ccg cag gtg cgc gac gtg ctg ctt tcc	480
Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser	
145 150 155 160	
ggc ggc gac ccg ctc aca ctc gcg ccg aag gtg ctg ggg cgc ctg ctt	528
Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu	
165 170 175	
tcc gaa ctt cgt aaa atc gag cac atc gaa atc atc cgc atc ggc acc	576
Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr	
180 185 190	
cgc gtg ccc gtg ttc atg ccc atg cgc gtg acc cag gaa ctg tgc gac	624
Arg Val Pro Val Phe Met Pro Met Arg Val Thr Gln Glu Leu Cys Asp	
195 200 205	
acg ctc gcc gaa cac cat ccg ctg tgg atg aac att cac gtc aac cac	672
Thr Leu Ala Glu His His Pro Leu Trp Met Asn Ile His Val Asn His	
210 215 220	
ccc aag gaa atc acc ccc gaa gtg gcc gag gcg tgt gac cgt ctg acc	720
Pro Lys Glu Ile Thr Pro Glu Val Ala Glu Ala Cys Asp Arg Leu Thr	
225 230 235 240	
cgc gcg ggc gtg ccg ctc ggc aac cag agc gtg ctg ctg cgc gcc gtg	768
Arg Ala Gly Val Pro Leu Gly Asn Gln Ser Val Leu Leu Arg Gly Val	
245 250 255	
aac gac cac ccg gtc atc atg caa aag ctg ctg cgc gag ctc gtc aaa	816
Asn Asp His Pro Val Ile Met Gln Lys Leu Leu Arg Glu Leu Val Lys	
260 265 270	
att cgg gtg cgc ccc tac tac atc tac cag tgc gac ctc gtg cac ggc	864
Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Val His Gly	
275 280 285	
gct ggg cac ctg cgc acc acg gtc agt aag ggt ctg gaa atc atg gaa	912
Ala Gly His Leu Arg Thr Thr Val Ser Lys Gly Leu Glu Ile Met Glu	
290 295 300	
tcg ctg cgc gcc cac acc tcc gcc tac agc gtg ccg acc tac gtg gtg	960
Ser Leu Arg Gly His Thr Ser Gly Tyr Ser Val Pro Thr Tyr Val Val	
305 310 315 320	

gac gcg ccc ggc ggc ggc ggc aag att ccg gtg gcg ccc aac tac gtg 1008  
 Asp Ala Pro Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val 335  
 325 330 335  
 ctc tcg cac agc cct gag aag ctg att ctg cgc aac ttc gag ggc tac 1056  
 Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr 350  
 340 345 350  
 atc gcc gcc tac tcg gag ccc acc gat tac acc ggc ccc gac atg gcg 1104  
 Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala 365  
 355 360 365  
 att cct gac gac tgg att cgc aag gaa ccc ggc cag acc ggc atc ttc 1152  
 Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe 380  
 370 375 380  
 ggc ctg atg gaa ggc gag cgc att tcc atc gag ccg 1188  
 Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro 395  
 385 390 395

<210> 12  
 <211> 396  
 <212> PRT  
 <213> Deinococcus radiodurans

<400> 12  
 Trp Gln Gly Val Pro Asp Glu Gln Trp Tyr Asp Trp Lys Trp Gln Leu  
 1 5 10 15  
 Lys Asn Arg Ile Asn Ser Val Glu Glu Leu Gln Glu Val Leu Thr Leu  
 20 25 30  
 Thr Glu Ser Glu Tyr Arg Gly Ala Ser Ala Glu Gly Ile Phe Arg Leu  
 35 40 45  
 Asp Ile Thr Pro Tyr Phe Ala Ser Leu Met Asp Pro Glu Asp Pro Thr  
 50 55 60  
 Cys Pro Val Arg Arg Gln Val Ile Pro Thr Glu Glu Glu Leu Gln Pro  
 65 70 75 80  
 Phe Thr Ser Met Met Glu Asp Ser Leu Ala Glu Asp Lys His Ser Pro  
 85 90 95  
 Val Pro Gly Leu Val His Arg Tyr Pro Asp Arg Val Leu Met Leu Val  
 100 105 110  
 Thr Thr Gln Cys Ala Ser Tyr Cys Arg Tyr Cys Thr Arg Ser Arg Ile  
 115 120 125  
 Val Gly Asp Pro Thr Glu Thr Phe Asn Pro Ala Glu Tyr Glu Ala Gln  
 130 135 140  
 Leu Asn Tyr Leu Arg Asn Thr Pro Gln Val Arg Asp Val Leu Leu Ser  
 145 150 155 160  
 Gly Gly Asp Pro Leu Thr Leu Ala Pro Lys Val Leu Gly Arg Leu Leu  
 165 170 175  
 Ser Glu Leu Arg Lys Ile Glu His Ile Glu Ile Ile Arg Ile Gly Thr  
 180 185 190

Arg Val Pro Val Phe Met Pro Met Arg Val Thr Gln Glu Leu Cys Asp  
 195 200 205  
 Thr Leu Ala Glu His His Pro Leu Trp Met Asn Ile His Val Asn His  
 210 215 220  
 Pro Lys Glu Ile Thr Pro Glu Val Ala Glu Ala Cys Asp Arg Leu Thr  
 225 230 235 240  
 Arg Ala Gly Val Pro Leu Gly Asn Gln Ser Val Leu Leu Arg Gly Val  
 245 250 255  
 Asn Asp His Pro Val Ile Met Gln Lys Leu Leu Arg Glu Leu Val Lys  
 260 265 270  
 Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Val His Gly  
 275 280 285  
 Ala Gly His Leu Arg Thr Thr Val Ser Lys Gly Leu Glu Ile Met Glu  
 290 295 300  
 Ser Leu Arg Gly His Thr Ser Gly Tyr Ser Val Pro Thr Tyr Val Val  
 305 310 315 320  
 Asp Ala Pro Gly Gly Gly Gly Lys Ile Pro Val Ala Pro Asn Tyr Val  
 325 330 335  
 Leu Ser His Ser Pro Glu Lys Leu Ile Leu Arg Asn Phe Glu Gly Tyr  
 340 345 350  
 Ile Ala Ala Tyr Ser Glu Pro Thr Asp Tyr Thr Gly Pro Asp Met Ala  
 355 360 365  
 Ile Pro Asp Asp Trp Ile Arg Lys Glu Pro Gly Gln Thr Gly Ile Phe  
 370 375 380  
 Gly Leu Met Glu Gly Glu Arg Ile Ser Ile Glu Pro  
 385 390 395

<210> 13  
 <211> 1113  
 <212> DNA  
 <213> Aquifex aeolicus

<220>  
 <221> CDS  
 <222> (1)..(1110)

<400> 13  
 atg cgt cgc ttt ttt gag aat gta ccg gaa aac ctc tgg agg agc tac 48  
 Met Arg Arg Phe Phe Glu Asn Val Pro Glu Asn Leu Trp Arg Ser Tyr  
 1 5 10 15  
 gag tgg cag ata caa aac agg ata aaa act ctt aag gag ata aaa aag 96  
 Glu Trp Gln Ile Gln Asn Arg Ile Lys Thr Leu Lys Glu Ile Lys Lys  
 20 25 30  
 tac tta aaa ctc ctt ccc gag gag gaa gaa gga att aaa aga act caa 144  
 Tyr Leu Lys Leu Leu Pro Glu Glu Glu Glu Gly Ile Lys Arg Thr Gln  
 35 40 45

ggg ctt tat ccc ttt gcg ata aca cct tac tac ctc tct tta ata aat 192  
 Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn  
 50 55 60

cca gag gac ccg aag gat cct ata aga ctt cag gca atc ccc cgc gtt 240  
 Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val  
 65 70 75 80

gta gaa gtt gat gaa aag gtt cag tct gcg gga gaa cca gac gct ctg 288  
 Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu  
 85 90 95

aaa gaa gaa gga gat att ccg ggt ctt aca cac agg tat ccc gac agg 336  
 Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg  
 100 105 110

gtt ctt tta aac gtc act acc ttt tgt gcg gtt tac tgc agg cac tgt 384  
 Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys  
 115 120 125

atg aga aag agg ata ttc tct cag ggt gag agg gca agg act aaa gag 432  
 Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu  
 130 135 140

gaa ata gac acg atg att gat tac ata aag aga cac gaa gag ata agg 480  
 Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg  
 145 150 155 160

gat gtc tta att tca ggt ggt gag cca ctt tcc ctt tcc ttg gaa aaa 528  
 Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys  
 165 170 175

ctt gaa tac tta ctc tca agg tta agg gaa ata aaa cac gtg gaa att 576  
 Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile  
 180 185 190

ata cgc ttt ggg acg agg ctt ccc gtt ctt gca ccc cag agg ttc ttt 624  
 Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe  
 195 200 205

aac gat aaa ctt ctg gac ata ctg gaa aaa tac tcc ccc ata tgg ata 672  
 Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile  
 210 215 220

aac act cac ttc aac cat ccg aat gag ata acc gag tac gcg gaa gaa 720  
 Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu  
 225 230 235 240

gcg gtg gac agg ctc ctg aga agg ggc att ccc gtg aac aac cag aca 768  
 Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr  
 245 250 255

gtc cta ctt aaa ggc gta aac gac gac cct gaa gtt atg cta aaa ctc 816  
 Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu  
 260 265 270

ttt aga aaa ctt tta agg ata aag gta aag ccc cag tac ctc ttt cac 864  
 Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His  
 275 280 285

tgc gac ccg ata aag gga gcg gtt cac ttt agg act acg ata gac aaa 912  
 Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys  
 290 295 300

gga ctt gaa ata atg aga tat ttg agg gga agg ctg agc ggt ttc ggg 960  
 Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly  
 305 310 315 320

ata ccc act tac gcg gtg gac ctc ccg gga ggg aaa ggt aag gtt cct 1008  
 Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro  
 325 330 335

ctt ctt ccc aac tac gta aag aaa agg aaa ggt aat aag ttc tgg ttt 1056  
 Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe  
 340 345 350

gaa agt ttc acg ggt gag gtc gta gaa tac gaa gta acg gaa gta tgg 1104  
 Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp  
 355 360 365

gaa cct tga 1113  
 Glu Pro  
 370

<210> 14  
 <211> 370  
 <212> PRT  
 <213> Aquifex aeolicus

<400> 14  
 Met Arg Arg Phe Phe Glu Asn Val Pro Glu Asn Leu Trp Arg Ser Tyr  
 1 5 10 15

Glu Trp Gln Ile Gln Asn Arg Ile Lys Thr Leu Lys Glu Ile Lys Lys  
 20 25 30

Tyr Leu Lys Leu Leu Pro Glu Glu Glu Gly Ile Lys Arg Thr Gln  
 35 40 45

Gly Leu Tyr Pro Phe Ala Ile Thr Pro Tyr Tyr Leu Ser Leu Ile Asn  
 50 55 60

Pro Glu Asp Pro Lys Asp Pro Ile Arg Leu Gln Ala Ile Pro Arg Val  
 65 70 75 80

Val Glu Val Asp Glu Lys Val Gln Ser Ala Gly Glu Pro Asp Ala Leu  
 85 90 95

Lys Glu Glu Gly Asp Ile Pro Gly Leu Thr His Arg Tyr Pro Asp Arg  
 100 105 110

Val Leu Leu Asn Val Thr Thr Phe Cys Ala Val Tyr Cys Arg His Cys  
 115 120 125

Met Arg Lys Arg Ile Phe Ser Gln Gly Glu Arg Ala Arg Thr Lys Glu  
 130 135 140

Glu Ile Asp Thr Met Ile Asp Tyr Ile Lys Arg His Glu Glu Ile Arg  
 145 150 155 160

Asp Val Leu Ile Ser Gly Gly Glu Pro Leu Ser Leu Ser Leu Glu Lys  
 165 170 175

Leu Glu Tyr Leu Leu Ser Arg Leu Arg Glu Ile Lys His Val Glu Ile  
 180 185 190

Ile Arg Phe Gly Thr Arg Leu Pro Val Leu Ala Pro Gln Arg Phe Phe  
195 200 205

Asn Asp Lys Leu Leu Asp Ile Leu Glu Lys Tyr Ser Pro Ile Trp Ile  
210 215 220

Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Tyr Ala Glu Glu  
225 230 235 240

Ala Val Asp Arg Leu Leu Arg Arg Gly Ile Pro Val Asn Asn Gln Thr  
245 250 255

Val Leu Leu Lys Gly Val Asn Asp Asp Pro Glu Val Met Leu Lys Leu  
260 265 270

Phe Arg Lys Leu Leu Arg Ile Lys Val Lys Pro Gln Tyr Leu Phe His  
275 280 285

Cys Asp Pro Ile Lys Gly Ala Val His Phe Arg Thr Thr Ile Asp Lys  
290 295 300

Gly Leu Glu Ile Met Arg Tyr Leu Arg Gly Arg Leu Ser Gly Phe Gly  
305 310 315 320

Ile Pro Thr Tyr Ala Val Asp Leu Pro Gly Gly Lys Gly Lys Val Pro  
325 330 335

Leu Leu Pro Asn Tyr Val Lys Lys Arg Lys Gly Asn Lys Phe Trp Phe  
340 345 350

Glu Ser Phe Thr Gly Glu Val Val Glu Tyr Glu Val Thr Glu Val Trp  
355 360 365

Glu Pro  
370

<210> 15  
<211> 1065  
<212> DNA  
<213> Treponema pallidum

<220>  
<221> CDS  
<222> (1)..(1065)

<400> 15  
atg tct atg gct gag tgt acc cgg gaa cag aga aag aga cga ggt gca 48  
Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala  
1 5 10 15

ggg cgt gct gat gag cat tgg cgg acg ttg agt cct gcc tct tgc gcg 96  
Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala  
20 25 30

gca gat gcg ctg acg gag cat att tct cca gcg tat gcg cat tta att 144  
Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile  
35 40 45

gca caa gcg cag ggc gcg gac gcg cag gcg ctg aaa cgt cag gtg tgc 192  
Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys  
50 55 60

ttt gcg cca cag gag cgt gtg gtg cat gct tgc gag tgt gcc gac cca	240
Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro	
65 70 75 80	
ttg ggt gag gac cgg tac tgc gtg aca ccc ttt ttg gtg cat cag tat	288
Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr	
85 90 95	
gcg aat cgt gtg ttg atg ttg gca aca gga cgt tgc ttt tca cac tgt	336
Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys	
100 105 110	
cgc tat tgt ttt cgc cgc ggt ttc atc gcc caa cgt gca ggg ttg atc	384
Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile	
115 120 125	
ccc aac gaa gag cgc gag aag att att acg tat ctt cgt gct acc cct	432
Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro	
130 135 140	
tgc gtg aag gaa atc ctg gtt tca ggt ggt gat cca ctc act ggt tct	480
Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser	
145 150 155 160	
ttt gca cag gtc aca tcg ctt ttc cgc gca ctg cgc agt gta gcg ccg	528
Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro	
165 170 175	
gat ttg att att cgt ctg tgc act cgc gca gtc acc ttt gct ccg cag	576
Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln	
180 185 190	
gcc ttt act ccc gag ctg att gcg ttt ctg cag gag atg aag ccg gtg	624
Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val	
195 200 205	
tggtg ata att ccg cat att aat cac ccg gca gag ctc ggt tct acg cag	672
Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln	
210 215 220	
cgc gcg gtg ctc gag gcc tgc gta ggc gca ggc ctc cct gtg caa tcg	720
Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser	
225 230 235 240	
cag tcg gta ctg ttg cgc ggg gtg aac gat tcg gta gag acg ctg tgc	768
Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys	
245 250 255	
aca ctg ttt cac gcg ctc act tgt ctg ggg gtt aag ccg ggg tat cta	816
Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu	
260 265 270	
ttt cag ttg gat ttg gcg cct gga act ggg gat ttt cgt gtg cca ctt	864
Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu	
275 280 285	
tct gac acg cta gct ctg tgg cgc aca ttg aag gag cgc ctc tca ggg	912
Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly	
290 295 300	
ttg tcg ctt ccc acg ctt gcg gtg gac ttg cca ggg ggt gga gga aag	960
Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Lys	
305 310 315 320	

ttt ccg ctt gtg gca ttg gcc ttg cag caa gat gtc acg tgg cat cag 1008  
 Phe Pro Leu Val Ala Leu Ala Leu Gln Gln Asp Val Thr Trp His Gln 335  
 325 330 335  
 gaa cgc gag cgc ttc tcc gca cgc gcc atc gat gcc cgc tgg tac acg 1056  
 Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr 350  
 340 345 350  
 tac ccg ttc 1065  
 Tyr Pro Phe 355

<210> 16  
 <211> 355  
 <212> PRT  
 <213> Treponema pallidum

<400> 16  
 Met Ser Met Ala Glu Cys Thr Arg Glu Gln Arg Lys Arg Arg Gly Ala  
 1 5 10 15  
 Gly Arg Ala Asp Glu His Trp Arg Thr Leu Ser Pro Ala Ser Cys Ala  
 20 25 30  
 Ala Asp Ala Leu Thr Glu His Ile Ser Pro Ala Tyr Ala His Leu Ile  
 35 40 45  
 Ala Gln Ala Gln Gly Ala Asp Ala Gln Ala Leu Lys Arg Gln Val Cys  
 50 55 60  
 Phe Ala Pro Gln Glu Arg Val Val His Ala Cys Glu Cys Ala Asp Pro  
 65 70 75 80  
 Leu Gly Glu Asp Arg Tyr Cys Val Thr Pro Phe Leu Val His Gln Tyr  
 85 90 95  
 Ala Asn Arg Val Leu Met Leu Ala Thr Gly Arg Cys Phe Ser His Cys  
 100 105 110  
 Arg Tyr Cys Phe Arg Arg Gly Phe Ile Ala Gln Arg Ala Gly Trp Ile  
 115 120 125  
 Pro Asn Glu Glu Arg Glu Lys Ile Ile Thr Tyr Leu Arg Ala Thr Pro  
 130 135 140  
 Ser Val Lys Glu Ile Leu Val Ser Gly Gly Asp Pro Leu Thr Gly Ser  
 145 150 155 160  
 Phe Ala Gln Val Thr Ser Leu Phe Arg Ala Leu Arg Ser Val Ala Pro  
 165 170 175  
 Asp Leu Ile Ile Arg Leu Cys Thr Arg Ala Val Thr Phe Ala Pro Gln  
 180 185 190  
 Ala Phe Thr Pro Glu Leu Ile Ala Phe Leu Gln Glu Met Lys Pro Val  
 195 200 205  
 Trp Ile Ile Pro His Ile Asn His Pro Ala Glu Leu Gly Ser Thr Gln  
 210 215 220  
 Arg Ala Val Leu Glu Ala Cys Val Gly Ala Gly Leu Pro Val Gln Ser  
 225 230 235 240



Gln Ser Val Leu Leu Arg Gly Val Asn Asp Ser Val Glu Thr Leu Cys  
 245 250 255  
 Thr Leu Phe His Ala Leu Thr Cys Leu Gly Val Lys Pro Gly Tyr Leu  
 260 265 270  
 Phe Gln Leu Asp Leu Ala Pro Gly Thr Gly Asp Phe Arg Val Pro Leu  
 275 280 285  
 Ser Asp Thr Leu Ala Leu Trp Arg Thr Leu Lys Glu Arg Leu Ser Gly  
 290 295 300  
 Leu Ser Leu Pro Thr Leu Ala Val Asp Leu Pro Gly Gly Gly Lys  
 305 310 315 320  
 Phe Pro Leu Val Ala Leu Ala Leu Gln Asp Val Thr Trp His Gln  
 325 330 335  
 Glu Arg Glu Ala Phe Ser Ala Arg Gly Ile Asp Gly Ala Trp Tyr Thr  
 340 345 350  
 Tyr Pro Phe  
 355

<210> 17  
 <211> 6  
 <212> PRT  
 <213> Clostridium subterminale

<400> 17  
 Lys Asp Val Ser Asp Ala  
 1 5

<210> 18  
 <211> 17  
 <212> DNA  
 <213> Clostridium subterminale

<220>  
 <221> modified\_base  
 <222> (9)  
 <223> n is inosine

<220>  
 <221> modified\_base  
 <222> (12)  
 <223> n is inosine

<400> 18  
 aargaygtnw engaygc

17

<210> 19  
 <211> 6  
 <212> PRT  
 <213> Clostridium subterminale

<400> 19  
 Gln Ser His Asp Lys Val  
 1 5

<210> 20  
 <211> 20  
 <212> DNA  
 <213> Clostridium subterminale

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> n is inosine

<220>  
 <221> modified\_base  
 <222> (15)  
 <223> n is inosine

<400> 20  
 atnacyttxt crtgnswytg

20

<210> 21  
 <211> 48  
 <212> PRT  
 <213> Clostridium subterminale

<400> 21  
 Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys Val Ile Leu Arg Asn  
 1 5 10 15

Phe Glu Gly Val Ile Thr Thr Tyr Ser Glu Pro Ile Asn Tyr Thr Pro  
 20 25 30

Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys Lys Val His Lys Val  
 35 40 45

<210> 22  
 <211> 15  
 <212> PRT  
 <213> Clostridium subterminale

<400> 22  
 Ala Leu Glu Pro Val Gly Leu Glu Arg Asn Lys Arg His Val Gln  
 1 5 10 15

<210> 23  
 <211> 16  
 <212> PRT  
 <213> Clostridium subterminale

<400> 23  
 Met Ile Asn Arg Arg Tyr Glu Leu Phe Lys Asp Val Ser Asp Ala Asp  
 1 5 10 15

<210> 24  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 24  
atcctaacga tcctaagatg cc 22

<210> 25  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 25  
tggatgggta aagtgaatg 19

<210> 26  
<211> 500  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Probe

<400> 26  
atcctaacga tcctaagatg ccagtaagaa aacaagctat tccaacagca ttagagctta 60  
acaaagctgc tgcagatctt gaagacccat tacatgaaga tacagattca ccagtacctg 120  
gattaactca cagatatcca gatagagtat tattattaat aactgatatg tgctcaatg 180  
actgcagaca ctgtacaaga agaagatttg caggacaaag cgatgactct atgccaatgg 240  
aaagaataga taaagctata gattatatca gaaatactcc tcaagttaga gacgtattat 300  
tatcaggtgg agacgctctt ttagtatctg atgaaacatt agaatacatc atagctaaat 360  
taagagaaat accacacggt gaaatagtaa gaataggttc aagaactcca gttgttcttc 420  
cacaaagaat aactccagaa cttgtaaata tgcttaaaaa atatcatcca gtatgggtaa 480  
aactcactt taaccatcca 500

<210> 27  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 27  
tacacatatg ataaatagaa gatatg 26

<210> 28  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 <400> 28  
 tagactcgag ttattcttga acgtgtctc 29  
  
 <210> 29  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 <400> 29  
 tacagaattc atgataata gaagatatg 29  
  
 <210> 30  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 <400> 30  
 tagaaagctt ttattcttga acgtgtctc 29  
  
 <210> 31  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 <400> 31  
 tataggatcc gaccgtataa ttcacgcgat tacacc 36  
  
 <210> 32  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
 <400> 32  
 tagagaattc gattcagtcg ggcgtcccat tacc 34